Sequence search alignment


```
RESULT 21
AAA13558/c
ID   AAA13558 standard; DNA; 14 BP.
XX
AC   AAA13558;
XX
DT   20-JUL-2000  (first entry)
XX
DE   CFTR gene exon 10 PCR primer CFEx10-R.
XX
KW   Cystic fibrosis; mutation; detection; mass spectrometry; diagnosis;
KW   genetic disease; chromosomal abnormality; infection; cancer; obesity;
KW   atherosclerosis; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   US6043031-A.
XX
PD   28-MAR-2000.
XX
PF   18-MAR-1996;   96US-00617256.
XX
PR   17-MAR-1995;   95US-00406199.
XX
PA   (SEQU-) SEQUENOM INC.
XX
PI   Koester H,  Higgens GS,  Little DP;
XX
DR   WPI; 2000-270337/23.
XX
PT   Identifying target nucleic acid sequence in a biological sample useful
PT   for diagnosis of genetic disease or chromosomal abnormality, involves
PT   using mass spectrometer.
XX
PS   Example 7; Col 28; 95pp; English.
XX
CC   The present invention describes a method developed for identifying a
CC   target nucleic acid sequence (NA) in a biological sample as normal or
CC   mutant, by hybridising the NA with a mutant or normal primer capable of
CC   hybridising to the mutated or wildtype sequence in the target NA and
CC   identifying the target NA by mass spectrometry. The method can be used
CC   for diagnosis of genetic disease, chromosomal abnormality, a
CC   predisposition to a genetic disease, cancer or an infection, by
CC   identifying a target nucleic acid sequence in a biological sample. The
CC   method is also useful for diagnosing a predisposition to a disease or
CC   condition (e.g. obesity, atherosclerosis) or to provide information
CC   relating to identity, heredity or compatibility (e.g. HLA phenotyping).
CC   The method is highly accurate, reliable and avoids electrophoretic,
CC   labeling and detection steps. The entire method can be completed within 2
CC   -3 hours and is less expensive. Nucleic acid fragments are identified and
CC   detected at the same time by the specific molecular weights and the
CC   method allows rigorous controls for preventing false negative or positive
CC   results. The present sequence represents a PCR primer for exon 10 of the
CC   CFTR gene which is used in an example from the present invention
XX
SQ   Sequence 14 BP; 2 A; 1 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match             47.8%;  Score 11;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches   11;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy          2 ACGCCCTTCAC 12
              ||||||||||
Db         13 ACGCCCTTCAC 3
```

Sequence Search alignment

RESULT 103
AAX77471/c
ID AAX77471 standard; DNA; 10 BP.
XX
AC AAX77471;
XX
DT 05-AUG-1999 (first entry)
XX
DE US5912147 primer 15.
XX
KW Primer; quantitation; genetic instability; tumour cell; detection;
KW neoplastic transformation; carcinogenesis; ss.
XX
OS Synthetic.
XX
PN US5912147-A.
XX
PD 15-JUN-1999.
XX
PF 22-OCT-1996; 96US-00734973.
XX
PR 22-OCT-1996; 96US-00734973.
XX
PA (HEAL-) HEALTH RES INC.

XX
PI Anderson G, Stoler D, Basik M;
XX
DR WPI; 1999-357197/30.
XX
PT Quantitating genetic instability.
XX
PS Claim 4; Col 21-22; 27pp; English.
XX
CC This invention describes a novel method for quantitating genetic
CC instability independent of microsatellite alterations by treating a
CC comparison pair comprising genomic DNA from tumour cells and genomic DNA
CC from normal cells. The method involves the cells from the same individual
CC with oligonucleotide primers selected from (i) a nucleotide sequence
CC (CG)xRG, where R is a purine selected from adenine and guanine and x = 3-
CC 7, (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and Y is a
CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
CC a nucleotide sequence (CG)xRR, where R is as in (i) and x = 3-7, (iv) a
CC nucleotide sequence (CG)xYY, where Y is a pyrimidine selected from
CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
CC (CA)xRG, where R is a purine selected from adenine and guanine and x = 6-
CC 16, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from
CC adenine and guanine and Y is a pyrimidine selected from cytosine,
CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR,
CC where R is a purine selected from adenine and guanine and x = 6-16,
CC (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected
CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
CC of the primers. The method is useful for detecting genomic instability
CC which are commonly associated with the various stages of neoplastic
XX transformation and carcinogenesis. The method is rapid and simple
SQ Sequence 10 BP; 0 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 36.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ACCGCGCGGG 20
    ||||||||| |
Db 10 ACCGCGCGCG 1